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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 12 Jan 105 12:57:02 PST

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

8. US-10-665-283-8 (1-1947)
1. US-10-665-283-1 (1-1927)
6. US-10-665-283-6 (1-1927)
4. US-10-665-283-4 (1-1891)

Region Alignment: (listed in Clustered order)

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US-10-665- 1 MALRGCSDGSDPLMDNVTWNTSNPDTKCFQNTLVWVPCFYLMACFPFYLYLSRHD
US-10-665- 1 MALRGCSDGSDPLMDNVTWNTSNPDTKCFQNTLVWVPCFYLMACFPFYLYLSRHD
US-10-665- 1 MALRGCSDGSDPLMDNVTWNTSNPDTKCFQNTLVWVPCFYLMACFPFYLYLSRHD
US-10-665- 1 MALRGCSDGSDPLMDNVTWNTSNPDTKCFQNTLVWVPCFYLMACFPFYLYLSRHD
consensus MALRGCSDGSDPLMDNVTWNTSNPDTKCFQNTLVWVPCFYLMACFPFYLYLSRHD

US-10-665- 62 RGYIQTPLNKTALGFLMWVCWADLFYSFWERSRGIFLAPVFLVSPDLLGITLLATF
US-10-665- 62 RGYIQTPLNKTALGFLMWVCWADLFYSFWERSRGIFLAPVFLVSPDLLGITLLATF
US-10-665- 62 RGYIQTPLNKTALGFLMWVCWADLFYSFWERSRGIFLAPVFLVSPDLLGITLLATF
US-10-665- 62 RGYIQTPLNKTALGFLMWVCWADLFYSFWERSRGIFLAPVFLVSPDLLGITLLATF
consensus RGYIQTPLNKTALGFLMWVCWADLFYSFWERSRGIFLAPVFLVSPDLLGITLLATF

US-10-665- 123 LIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLL
US-10-665- 123 LIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLL
US-10-665- 123 LIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLL
US-10-665- 123 LIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLL
consensus LIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLL

US-10-665- 184 IQLVLSCFSDRSPLFSETIHDNPNCPRESSASFLSRITFWITGLIVRGYRQPLEGSDLWSL
US-10-665- 184 IQLVLSCFSDRSPLFSETIHDNPNCPRESSASFLSRITFWITGLIVRGYRQPLEGSDLWSL
US-10-665- 184 IQLVLSCFSDRSPLFSETIHDNPNCPRESSASFLSRITFWITGLIVRGYRQPLEGSDLWSL

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Search Notes

Amino acids 1-1531 (MDR)
= SEQ ID NO:4 of 5,766,880
(for example)
of A W S 7 4 8 6
1532-1537 = 6 gname spacer

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US-10-665- 184 IQLVLSCFSDRSPLFSETIHDNPNCPRESSASFLSRITFWITGLIVRGYRQPLEGSDLWSL
consensus IQLVLSCFSDRSPLFSETIHDNPNCPRESSASFLSRITFWITGLIVRGYRQPLEGSDLWSL

US-10-665- 245 NKEDTSEQVVPVLVKWKKCECAKTRKQPVKVYSSKDPAPKPKSSKVDANEVEALIVKSP
US-10-665- 245 NKEDTSEQVVPVLVKWKKCECAKTRKQPVKVYSSKDPAPKPKSSKVDANEVEALIVKSP
US-10-665- 245 NKEDTSEQVVPVLVKWKKCECAKTRKQPVKVYSSKDPAPKPKSSKVDANEVEALIVKSP
US-10-665- 245 NKEDTSEQVVPVLVKWKKCECAKTRKQPVKVYSSKDPAPKPKSSKVDANEVEALIVKSP
consensus NKEDTSEQVVPVLVKWKKCECAKTRKQPVKVYSSKDPAPKPKSSKVDANEVEALIVKSP

US-10-665- 306 QKEWNPSLFKVLYKTGPGYFLMSFFPKAIHDLAMFSGPQILKLLIKFVNDTKAPDMQGYFY
US-10-665- 306 QKEWNPSLFKVLYKTGPGYFLMSFFPKAIHDLAMFSGPQILKLLIKFVNDTKAPDMQGYFY
US-10-665- 306 QKEWNPSLFKVLYKTGPGYFLMSFFPKAIHDLAMFSGPQILKLLIKFVNDTKAPDMQGYFY
US-10-665- 306 QKEWNPSLFKVLYKTGPGYFLMSFFPKAIHDLAMFSGPQILKLLIKFVNDTKAPDMQGYFY
consensus QKEWNPSLFKVLYKTGPGYFLMSFFPKAIHDLAMFSGPQILKLLIKFVNDTKAPDMQGYFY

US-10-665- 367 TVLLFVTAQTLVLHGYFHI CFVSGMRIRITAVIGAYRKALVITNSARKSSTVGEIVNLM
US-10-665- 367 TVLLFVTAQTLVLHGYFHI CFVSGMRIRITAVIGAYRKALVITNSARKSSTVGEIVNLM
US-10-665- 367 TVLLFVTAQTLVLHGYFHI CFVSGMRIRITAVIGAYRKALVITNSARKSSTVGEIVNLM
US-10-665- 367 TVLLFVTAQTLVLHGYFHI CFVSGMRIRITAVIGAYRKALVITNSARKSSTVGEIVNLM
consensus TVLLFVTAQTLVLHGYFHI CFVSGMRIRITAVIGAYRKALVITNSARKSSTVGEIVNLM

US-10-665- 428 SVDQRPFMDLATYINMIWSAPLOVILALYLLWNLGSPVLGAVAVMLVMPVNAVMAKTK
US-10-665- 428 SVDQRPFMDLATYINMIWSAPLOVILALYLLWNLGSPVLGAVAVMLVMPVNAVMAKTK
US-10-665- 428 SVDQRPFMDLATYINMIWSAPLOVILALYLLWNLGSPVLGAVAVMLVMPVNAVMAKTK
US-10-665- 428 SVDQRPFMDLATYINMIWSAPLOVILALYLLWNLGSPVLGAVAVMLVMPVNAVMAKTK
consensus SVDQRPFMDLATYINMIWSAPLOVILALYLLWNLGSPVLGAVAVMLVMPVNAVMAKTK

US-10-665- 489 TYQVAHMKSKDNRIKLMNEILNGIKVLKYAWELAFKDKVLAIRQELKVLKKSAYLSAVG
US-10-665- 489 TYQVAHMKSKDNRIKLMNEILNGIKVLKYAWELAFKDKVLAIRQELKVLKKSAYLSAVG
US-10-665- 489 TYQVAHMKSKDNRIKLMNEILNGIKVLKYAWELAFKDKVLAIRQELKVLKKSAYLSAVG
US-10-665- 489 TYQVAHMKSKDNRIKLMNEILNGIKVLKYAWELAFKDKVLAIRQELKVLKKSAYLSAVG
consensus TYQVAHMKSKDNRIKLMNEILNGIKVLKYAWELAFKDKVLAIRQELKVLKKSAYLSAVG

US-10-665- 550 TFTWCTPFLVALCTFAVYVITDENNIIDAOQAFVSLALFNILRPLNLPVMSIIVQAS
US-10-665- 550 TFTWCTPFLVALCTFAVYVITDENNIIDAOQAFVSLALFNILRPLNLPVMSIIVQAS
US-10-665- 550 TFTWCTPFLVALCTFAVYVITDENNIIDAOQAFVSLALFNILRPLNLPVMSIIVQAS
US-10-665- 550 TFTWCTPFLVALCTFAVYVITDENNIIDAOQAFVSLALFNILRPLNLPVMSIIVQAS
consensus TFTWCTPFLVALCTFAVYVITDENNIIDAOQAFVSLALFNILRPLNLPVMSIIVQAS

US-10-665- 611 VSLKRLRIPLSHHELPDSIERRPVKGGGTNSITVRNATFTWASDPPLNGITFISIEG

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US-10-665- 611 VSLKRLRIFLSHEELEDPSIERRPVKDGCGGNTSITVRNATPTWARSDDPTLINGITPSIPG
US-10-665- 611 VSLKRLRIFLSHEELEDPSIERRPVKDGCGGNTSITVRNATPTWARSDDPTLINGITPSIPG
US-10-665- 611 VSLKRLRIFLSHEELEDPSIERRPVKDGCGGNTSITVRNATPTWARSDDPTLINGITPSIPG
consensus
US-10-665- 672 ALVAVGVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQAWIQNDSIRENILFGCOL
US-10-665- 672 ALVAVGVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQAWIQNDSIRENILFGCOL
US-10-665- 672 ALVAVGVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQAWIQNDSIRENILFGCOL
US-10-665- 672 ALVAVGVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQAWIQNDSIRENILFGCOL
consensus
US-10-665- 733 EEPYRSVIOACALLPDLIELPSGDRTEIGKGNLGGQKQKORVSLARAVYSNADIYLFDD
US-10-665- 733 EEPYRSVIOACALLPDLIELPSGDRTEIGKGNLGGQKQKORVSLARAVYSNADIYLFDD
US-10-665- 733 EEPYRSVIOACALLPDLIELPSGDRTEIGKGNLGGQKQKORVSLARAVYSNADIYLFDD
US-10-665- 733 EEPYRSVIOACALLPDLIELPSGDRTEIGKGNLGGQKQKORVSLARAVYSNADIYLFDD
consensus
US-10-665- 794 PLSAVDAHVGKHI FENVIGPKGMLKNKTRILVTHSMSYLPQVDVII VMSGGKISEMGSYOE
US-10-665- 794 PLSAVDAHVGKHI FENVIGPKGMLKNKTRILVTHSMSYLPQVDVII VMSGGKISEMGSYOE
US-10-665- 794 PLSAVDAHVGKHI FENVIGPKGMLKNKTRILVTHSMSYLPQVDVII VMSGGKISEMGSYOE
US-10-665- 794 PLSAVDAHVGKHI FENVIGPKGMLKNKTRILVTHSMSYLPQVDVII VMSGGKISEMGSYOE
consensus
US-10-665- 855 LLARDGAPAEFLRTYASTEQQDAEENGVTGSGPGKEAKQWENGMLVTDTSAGKOLQRLS
US-10-665- 855 LLARDGAPAEFLRTYASTEQQDAEENGVTGSGPGKEAKQWENGMLVTDTSAGKOLQRLS
US-10-665- 855 LLARDGAPAEFLRTYASTEQQDAEENGVTGSGPGKEAKQWENGMLVTDTSAGKOLQRLS
US-10-665- 855 LLARDGAPAEFLRTYASTEQQDAEENGVTGSGPGKEAKQWENGMLVTDTSAGKOLQRLS
consensus
US-10-665- 916 SSSSYSGDISRHNSHNSAELOKAEAKKEETWKLMEADKAQTQGVKLSVYVMDYMKAILGIFISF
US-10-665- 916 SSSSYSGDISRHNSHNSAELOKAEAKKEETWKLMEADKAQTQGVKLSVYVMDYMKAILGIFISF
US-10-665- 916 SSSSYSGDISRHNSHNSAELOKAEAKKEETWKLMEADKAQTQGVKLSVYVMDYMKAILGIFISF
US-10-665- 916 SSSSYSGDISRHNSHNSAELOKAEAKKEETWKLMEADKAQTQGVKLSVYVMDYMKAILGIFISF
consensus
US-10-665- 977 LSIPLFMCNHYVSALASNYWLSLWTDPIVNGTQEHKTVRLSVYGALGISQGIIVFGYSMAV
US-10-665- 977 LSIPLFMCNHYVSALASNYWLSLWTDPIVNGTQEHKTVRLSVYGALGISQGIIVFGYSMAV
US-10-665- 977 LSIPLFMCNHYVSALASNYWLSLWTDPIVNGTQEHKTVRLSVYGALGISQGIIVFGYSMAV
US-10-665- 977 LSIPLFMCNHYVSALASNYWLSLWTDPIVNGTQEHKTVRLSVYGALGISQGIIVFGYSMAV
consensus

US-10-665- 1038 SIGGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRRFSKELDTVDVSMIPEVIKMFMSGL
US-10-665- 1038 SIGGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRRFSKELDTVDVSMIPEVIKMFMSGL
US-10-665- 1038 SIGGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRRFSKELDTVDVSMIPEVIKMFMSGL
US-10-665- 1038 SIGGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRRFSKELDTVDVSMIPEVIKMFMSGL
consensus
US-10-665- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRFYVASSRQLKRLSVSRSPVYSHFNETL
US-10-665- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRFYVASSRQLKRLSVSRSPVYSHFNETL
US-10-665- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRFYVASSRQLKRLSVSRSPVYSHFNETL
US-10-665- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRFYVASSRQLKRLSVSRSPVYSHFNETL
consensus
US-10-665- 1160 LGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665- 1160 LGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665- 1160 LGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665- 1160 LGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665- 1160 LGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVI
consensus
US-10-665- 1221 SRHLSAGLVGLSVSYSLQVTTYLNWLVRMSSEMETNI VAVERLKEYSETEKEAPWQIQET
US-10-665- 1221 SRHLSAGLVGLSVSYSLQVTTYLNWLVRMSSEMETNI VAVERLKEYSETEKEAPWQIQET
US-10-665- 1221 SRHLSAGLVGLSVSYSLQVTTYLNWLVRMSSEMETNI VAVERLKEYSETEKEAPWQIQET
US-10-665- 1221 SRHLSAGLVGLSVSYSLQVTTYLNWLVRMSSEMETNI VAVERLKEYSETEKEAPWQIQET
consensus
US-10-665- 1282 APPSSWPQVGRVEFRNYCLRYREDLDFVLRIHINVTINGGKVGIVGRTGAGKSSLTGLGFR
US-10-665- 1282 APPSSWPQVGRVEFRNYCLRYREDLDFVLRIHINVTINGGKVGIVGRTGAGKSSLTGLGFR
US-10-665- 1282 APPSSWPQVGRVEFRNYCLRYREDLDFVLRIHINVTINGGKVGIVGRTGAGKSSLTGLGFR
US-10-665- 1282 APPSSWPQVGRVEFRNYCLRYREDLDFVLRIHINVTINGGKVGIVGRTGAGKSSLTGLGFR
consensus
US-10-665- 1343 INESAGEIIIDGINIAKIGLHDLRPFKTIIPDPVLFSGSLRMNLDPPFSQYDDEEVWTSI
US-10-665- 1343 INESAGEIIIDGINIAKIGLHDLRPFKTIIPDPVLFSGSLRMNLDPPFSQYDDEEVWTSI
US-10-665- 1343 INESAGEIIIDGINIAKIGLHDLRPFKTIIPDPVLFSGSLRMNLDPPFSQYDDEEVWTSI
US-10-665- 1343 INESAGEIIIDGINIAKIGLHDLRPFKTIIPDPVLFSGSLRMNLDPPFSQYDDEEVWTSI
consensus
US-10-665- 1404 ELAHLKDFVSALPKLDHECAEGENLSVGORQLVCLARALLRKTILVLDEATAAVDLET
US-10-665- 1404 ELAHLKDFVSALPKLDHECAEGENLSVGORQLVCLARALLRKTILVLDEATAAVDLET
US-10-665- 1404 ELAHLKDFVSALPKLDHECAEGENLSVGORQLVCLARALLRKTILVLDEATAAVDLET

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US-10-665- 1404 ELAHLKDFVSALPDKLDHECAGGENLSVGQQLVCLARALKTKIILVDEATAVDLET
consensus
US-10-665- 1465 DDLIOSTIRTPEDCTVLTIAHRLNTIMDYTRVILDKGEIQEYGAPSDLLQORGLFYFMA
US-10-665- 1465 DDLIOSTIRTPEDCTVLTIAHRLNTIMDYTRVILDKGEIQEYGAPSDLLQORGLFYFMA
US-10-665- 1465 DDLIOSTIRTPEDCTVLTIAHRLNTIMDYTRVILDKGEIQEYGAPSDLLQORGLFYFMA
US-10-665- 1465 DDLIOSTIRTPEDCTVLTIAHRLNTIMDYTRVILDKGEIQEYGAPSDLLQORGLFYFMA
consensus
US-10-665- 1526 KDAGLVGGGGGMLSRKGIIPPEYVLTRLAEDPAEPYRTRERRARFVSKKGCNCNVAHKNI
US-10-665- 1526 KDAGLVGGGGGMLSRKGIIPPEYVLTRLAEDPAEPYRTRERRARFVSKKGCNCNVAHKNI
US-10-665- 1526 KDAGLVGGGGGMLSRKGIIPPEYVLTRLAEDPAEPYRTRERRARFVSKKGCNCNVAHKNI
US-10-665- 1526 KDAGLVGGGGGMLSRKGIIPPEYVLTRLAEDPAEPYRTRERRARFVSKKGCNCNVAHKNI
consensus
US-10-665- 1587 REQGRFLQDVFTTLVDLKWPHLTLLIFTMSFLCSWLLFAMVWMLIAFAHGDlyaymekgtd
US-10-665- 1587 REQGRFLQDVFTTLVDLKWPHLTLLIFTMSFLCSWLLFAMVWMLIAFAHGD
US-10-665- 1587 REQGRFLQDVFTTLVDLKWPHLTLLIFTMSFLCSWLLFAMVWMLIAFAHGD
US-10-665- 1587 REQGRFLQDVFTTLVDLKWPHLTLLIFTMSFLCSWLLFAMVWMLIAFAHGD
consensus
US-10-665- 1648 LAPYpydvpdyagEGTNVPCVTSIHSFSSAFLESIEVQVTIGFGRMVTEECPLAILILIV
US-10-665- 1638 AP GEGTNVPCVTSIHSFSSAFLESIEVQVTIGFGRMVTEECPLAILILIV
US-10-665- 1638 AP GEGTNVPCVTSIHSFSSAFLESIEVQVTIGFGRMVTEECPLAILILIV
US-10-665- 1638 AP GEGTNVPCVTSIHSFSSAFLESIEVQVTIGFGRMVTEECPLAILILIV
consensus
US-10-665- 1709 QNIVGLMINAIMGCIIPMKTQAARRAETLIFSKHAVITILRHGRLCFMLRVGDLRKSMIIS
US-10-665- 1689 QNIVGLMINAIMGCIIPMKTQAARRAETLIFSKHAVITILRHGRLCFMLRVGDLRKSMIIS
US-10-665- 1689 QNIVGLMINAIMGCIIPMKTQAARRAETLIFSKHAVITILRHGRLCFMLRVGDLRKSMIIS
US-10-665- 1689 QNIVGLMINAIMGCIIPMKTQAARRAETLIFSKHAVITILRHGRLCFMLRVGDLRKSMIIS
consensus
US-10-665- 1770 ATIHMQVVRKTTSPGEVVPVPLHQVDIPMENGVGNGIFLVAPLIIVHVIDSNSPLYDLAPS
US-10-665- 1750 ATIHMQVVRKTTSPGEVVPVPLHQVDIPMENGVGNGIFLVAPLIIVHVIDSNSPLYDLAPS
US-10-665- 1750 ATIHMQVVRKTTSPGEVVPVPLHQVDIPMENGVGNGIFLVAPLIIVHVIDSNSPLYDLAPS
US-10-665- 1750 ATIHMQVVRKTTSPGEVVPVPLHQVDIPMENGVGNGIFLVAPLIIVHVIDSNSPLYDLAPS
consensus
US-10-665- 1831 DLHHQDLEIIIVILEGVVETGTTQARTSYLADEILWGQRFVPIVAEEDGRYSVDYSKFG
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US-10-665- 1811 DLHHQDLEIIIVILEGVVETGTTQARTSYLADEILWGQRFVPIVAEEDGRYSVDYSKFG
US-10-665- 1811 DLHHQDLEIIIVILEGVVETGTTQARTSYLADEILWGQRFVPIVAEEDGRYSVDYSKFG
US-10-665- 1811 DLHHQDLEIIIVILEGVVETGTTQARTSYLADEILWGQRFVPIVAEEDGRYSVDYSKFG
consensus
US-10-665- 1892 NTIKVPTPLCTARQLDEDRSLLDALTILASSRGPLRKRSVAVAKAKPKFSISPSLS
US-10-665- 1872 NTIKVPTPLCTARQLDEDRSLLDALTILASSRGPLRKRSVAVAKAKPKFSISPSLS
US-10-665- 1872 NTIKVPTPLCTARQLDEDRSLLDALTILASSRGPLRaaSVAVAKAKPKFSISPSLS
US-10-665- 1872 NTIKVPTPLCTARQLDEDRS
consensus
NTIKVPTPLCTARQLDEDRSllaldtlasrgplrkrsavakakpkfsispsdals
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Alignment score = 5263.00

Scoring matrix:

	1	4	6	8
1				
4	1711	1925	1827	
6		1711	1611	1825
8				

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